

(FILE 'HOME' ENTERED AT 10:16:33 ON 17 MAY 2002)

FILE 'REGISTRY' ENTERED AT 10:16:50 ON 17 MAY 2002

ENGVC CG/SEQP

E1 1 NGVAKLET/SEQP
E2 1 NGVAQEPVHLDSPA/K/SEQP
E3 0--> NGVCCG/SEQP
E4 1 NGVCCGAAA-AAALCH/AAAC/SEQP
E5 1 NGVCCGWLCHHYPC/SEQP
E6 3 NGVCCGYKLCHHYP/C/SEQP
E7 1 NGVCCGYKLCHORN/C/SEQP
E8 1 NGVCCGYKLCHPC/SEQP
E9 1 NGVCFYCFD/SEQP
E10 1 NGVCWTVV/SEQP
E11 1 NGVCWTVVH/SEQP
E12 1 NGVCWTVVHGA/SEQP

L1 9 S NGVCCG/SEQP

FILE 'CA' ENTERED AT 10:18:35 ON 17 MAY 2002

L2 5 SL1

FILE 'REGISTRY' ENTERED AT 10:20:33 ON 17 MAY 2002

ENGVC CGYKLCH/SEQP

E1 1 NGVCCGAAA-AAALCH/AAAC/SEQP
E2 1 NGVCCGWLCHHYP/C/SEQP
E3 0--> NGVCCGYKLCH/SEQP
E4 3 NGVCCGYKLCHHYP/C/SEQP
E5 1 NGVCCGYKLCHORN/C/SEQP
E6 1 NGVCCGYKLCHPC/SEQP
E7 1 NGVCFYCFD/SEQP
E8 1 NGVCWTVV/SEQP
E9 1 NGVCWTVVH/SEQP
E10 1 NGVCWTVVHGA/SEQP
E11 1 NGVCWTVVHGA GSKTLA GPKGPITQMYTNVDQDLV GWPAPP/SEQP
E12 1 NGVCWTVVHGA GTRTASPKGPVIQMYTNVDQDLV GWPAPQGSRLTPTCCSS
DLYLVTRHADVPVRRRGDSRGSLLSPRPISYLKSSSGPRLCPAGH/SEQP

L3 3 SE4
L4 1 SE5

FILE 'CA' ENTERED AT 10:22:15 ON 17 MAY 2002

L5 4 SL3
L6 1 SL4
L7 904885 S MAR?
L8 2734 S CONUS OR CONOTOX? OR CONOPEP?
L9 410 SL7 AND L8
L10 14197 S MAR OR MARI
L11 1 SL8 AND L10
L12 1512 S MARMOR?
L13 19 S L12 AND L8 NOT L10

L2 ANSWER 1 OF 5 CA COPYRIGHT 2002 ACS AN 136:48322 CA

TI Two new classes of conopeptides inhibit the α 1A β -adrenoceptor and noradrenaline transporter
AU Sharpe, Iain A.; Gehrmann, John; Loughnan, Merton L.; Thomas, Linda; Adams, Denise A.; Atkins, Ann; Palant, Elka; Craik, David J.; Adams, David J.; Alewood, Paul F.; Lewis, Richard J.
CS Institute for Molecular Bioscience, University of Queensland, Brisbane, 4072, Australia

SO Nature Neuroscience (2001), 4(9), 902-907 CODEN: NANEFN; ISSN: 1097-6256 PB Nature America Inc. DT Journal LA English

AB Cone snails use venom containing a cocktail of peptides (conopeptides) to capture their prey. Many of these peptides also target mammalian receptors, often with exquisite selectivity. Here we report the discovery of two new classes of conopeptides. One class targets α 1A β -adrenoceptors (p-TIA from the fish-hunting *Conus tulipa*), and the second class targets the neuronal noradrenaline transporter (ch1-Mrta and ch1-MrtaB from the mollusk-hunting *C. marmoreus*). α 1A-Mrta and ch1-Mrta selectively modulate these important membrane-bound proteins. Both peptides act as reversible non-competitive inhibitors and provide alternative avenues for the identification of inhibitor drugs.
RE CNT 38 THERE ARE 38 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 2 OF 5 CA COPYRIGHT 2002 ACS AN 134:189297 CA

TI λ -banda-Conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding: isolation and characterization from the venom of *Conus marmoreus*

AU Balaji, R. Ashok; Ohtake, Sato, Kazuki; Gopalakrishnakone, P.; Kini, R. Manjunatha; Seow, Kah Tong; Bay, Boon-Huat

CS Venom and Toxin Research Programme, Faculty of Medicine, National University of Singapore, Singapore, 117597, Singapore

SO Journal of Biological Chemistry (2000), 275(50), 39516-39522 CODEN: JBCHA3; ISSN: 0021-9258 PB American Society for Biochemistry and Molecular Biology DT Journal LA English

AB Conotoxins are multiple disulfide-bonded peptides isolated from marine cone snail venom. These toxins have been classified into several families based on their disulfide pattern and biol. properties. Here, the authors report a new family of *Conus* peptides, which have a novel cysteine motif. Three peptides of this family (Cm α VIA, Cm α VIB, and Cm α X) have been purified from *Conus marmoreus* venom, and their structures have been determined. Their amino acid sequences are VCCGYKLCHOC (Cm α VIA), NGVCCGYKLCHOC (Cm α VIB), and GICCGVSFCYOC (Cm α X), where O represents 4-trans-hydroxyproline. Two of these peptides (Cm α VIA and Cm α X) have been chem. synthesized. Using a selective protection and deprotection strategy during disulfide bond formation, peptides with both feasible cysteine-pairing combinations were generated. The disulfide pattern (C1-C4, C2-C3) in native toxins was identified by their co-elution with the synthetic disulfide-isomeric peptides on reverse-phase HPLC. Although cysteine residues were found in comparable positions with those of α 1A-conotoxins, these toxins exhibited a distinctly different disulfide bonding pattern; the authors have named this new family " λ -banda-conotoxins." Cm α VIA and Cm α X induced different biol. effects when injected intra-cerebroventricularly in mice: Cm α VIA induces seizures, whereas Cm α X induces flaccid paralysis. The synthetic peptide with λ -banda-conotoxin folding is about 1150-fold more potent in inducing seizures than the mispaired isomer with α 1A-conotoxin folding. Thus it appears that the unique disulfide pattern, and hence the "ribbons" conformation, in λ -banda-conotoxins is important for their biol. activity. RE CNT 21 THERE ARE 21 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 3 OF 5 CA COPYRIGHT 2002 ACS AN 134:82039 CA

TI Isolation and characterization of a novel *Conus* peptide with apparent antinociceptive activity

AU Melchish, J. Michael; Cornuz, Gloria O.; Layer, Richard T.; Garrett, James E.; Wagstaff, John D.; Buiel, Grzegorz; Wlazowka, Alexandra; Yoshikami, Doju; Cruz, Lourdes J.; Olivera, Baidomero M.

CS Departments of Psychiatry and Biology, University of Utah, Salt Lake City, UT, 84112, USA
SO Journal of Biological Chemistry (2000), 275(42), 32391-32397 CODEN: JBCHA3; ISSN: 0021-9258 PB American Society for Biochemistry and Molecular Biology DT Journal LA English

AB Cone snails are tropical marine mollusks that venomate prey with a complex mixt. of neuropharmacol. active compds. The authors report the discovery and biochem. characterization of a structurally unique peptide isolated from the venom of *Conus marmoreus*. The new peptide, m α 10a, potently increased withdrawal latency in a hot plate assay (a test of analgesia) at intrathecal doses that do not produce motor impairment as measured by rotarod test. The sequence of m α 10a is NGVCCGYKLCHOC, where O is 4-trans-hydroxyproline. This sequence is highly divergent from all other known conotoxins. Anal. of a cDNA clone encoding the toxin, however, indicates that it is a member of the recently described T-superfamily. Total chem. synthesis of the three possible disulfide arrangements of m α 10a was achieved, and elution studies indicate that the native form has a disulfide connectivity of Cys1-Cys4 and Cys2-Cys3. This disulfide linkage is unprecedented among conotoxins and defines a new family of *Conus* peptides. RE CNT 65 THERE ARE 65 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE FORMAT

L2 ANSWER 4 OF 5 CA COPYRIGHT 2002 ACS AN 133:131094 CA

TI Conotoxin peptides and their use as analgesics

IN McIntosh, J. Michael; Olivera, Baidomero M.; Cruz, Lourdes J.

PA University of Utah Research Foundation, USA

SO PCT Int. Appl., 29 pp. CODEN: PIXXD2 DT Patent LA English
FAN CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE
PI WO 2000/044769 A1 20000803 WO 2000-US1978 20000128 W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR,

LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG

PRAI US 1999-118381P P 19990129 US 1999-173343P P 19991228

AB The invention relates to relatively short peptides (termed ap-conotoxins herein), about 10-20 residues in length, which are naturally available in minute amounts in the venom of cone snails or analogous to the naturally available peptides, and which preferably include two disulfide bonds. These conotoxin peptides have analgesic activity and are thus useful for treating or preventing pain. Thus, the cDNA encoding the Conus marmoreus Marl1 propeptide was cloned and the analgesic activity of Marl1 and Marl2 was demonstrated in mice. RE.CNT 2 THERE ARE 2 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE.FORMAT

L2 ANSWER 5 OF 5 CA COPYRIGHT 2002 ACS AN 132-288779 CA

T1 Recombinant, chi-conotoxin peptides for inhibiting neuronal amine transporters

IN Lewis, Richard James; Alewood, Paul Francis; Sharpe, Iain Andrew

PA The University of Queensland, Australia

SO PCT Int. Appl. 47 pp. CODEN: PIXXD2 DT Patent LA English

FAN.CNT 1 PATENT NO. KIND DATE APPLICATION NO. DATE _____

PI WO 2000020444 A1 20000413 WO 1999-AU844 19991001 W: AE, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CR, CU, CZ, DE, DK, DM, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM, RW: GH, GM, KE, LS, MW, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG AU 9964530 A1 20000426 AU 1999-64530 19991001 EP 1117682 A1 20010725 EP 1999-962156 19991001 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, SI, LT, LV, FI, RO PRAI AU 1998-6274 A 19981002 WO 1999-AU844 W 19991001

AB The invention relates to an isolated, synthetic or recombinant <<chi-conotoxin peptide having the ability to inhibit a neuronal amine transporter, nucleic acid moieties encoding all or part of such peptides, antibodies to such peptides and uses and methods of treatment involving them. RE.CNT 1 THERE ARE 1 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE RE.FORMAT

L5 ANSWER 1 OF 4 CA COPYRIGHT 2002 ACS

T1 Two new classes of conopeptides inhibit the alpha-1-adrenoceptor and noradrenaline transporter PY 2001

L5 ANSWER 2 OF 4 CA COPYRIGHT 2002 ACS

T1 lambda-Conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding: isolation and characterization from the venom of Conus marmoreus PY 2000

L5 ANSWER 3 OF 4 CA COPYRIGHT 2002 ACS

T1 Isolation and characterization of a novel Conus peptide with apparent antinociceptive activity PY 2000

L5 ANSWER 4 OF 4 CA COPYRIGHT 2002 ACS

T1 Conotoxin peptides and their use as analgesics PY 2000

L6 ANSWER 1 OF 1 CA COPYRIGHT 2002 ACS

T1 Recombinant, chi-conotoxin peptides for inhibiting neuronal amine transporters PY 2000 2000 2001

L11 ANSWER 1 OF 1 CA COPYRIGHT 2002 ACS

T1 Conotoxin peptides and their use as analgesics PY 2000

L13 ANSWER 1 OF 19 CA COPYRIGHT 2002 ACS

T1 New members of the .mu.-conotoxin family for use in the treatment of disease associated with sodium channel function and cDNAs encoding them PY 2002

L13 ANSWER 2 OF 19 CA COPYRIGHT 2002 ACS

T1 Two new classes of conopeptides inhibit the alpha-1-adrenoceptor and noradrenaline transporter PY 2001

L13 ANSWER 3 OF 19 CA COPYRIGHT 2002 ACS

T1 O-superfamily conotoxin peptides and cDNAs and pharmaceutical uses PY 2001

L13 ANSWER 4 OF 19 CA COPYRIGHT 2002 ACS

T1 Disulfide bond pattern of a lambda-conotoxin, a novel toxin from Conus Marmoreus PY 2001

L13 ANSWER 5 OF 19 CA COPYRIGHT 2002 ACS

T1 lambda-Conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding: isolation and characterization from the venom of Conus marmoreus PY 2000

L13 ANSWER 6 OF 19 CA COPYRIGHT 2002 ACS

T1 Isolation and characterization of a novel Conus peptide with apparent antinociceptive activity PY 2000

L13 ANSWER 7 OF 19 CA COPYRIGHT 2002 ACS

T1 tau-conotoxin peptides and cDNAs and pharmaceuticals containing tau-conotoxin peptides PY 2000 2001

L13 ANSWER 8 OF 19 CA COPYRIGHT 2002 ACS

T1 Alpha-conotoxins and nucleic acids encoding them PY 2000 2001

L13 ANSWER 9 OF 19 CA COPYRIGHT 2002 ACS

T1 Structural Differences in the Two Agonist Binding Sites of the Torpedo Nicotinic Acetylcholine Receptor Revealed by Time-Resolved Fluorescence Spectroscopy PY 2000

L13 ANSWER 10 OF 19 CA COPYRIGHT 2002 ACS

T1 The strategy used by some piscivorous cone snails to capture their prey: the effects of their venoms on vertebrates and on isolated neuromuscular preparations PY 1999

L13 ANSWER 11 OF 19 CA COPYRIGHT 2002 ACS

T1 Isolation, structure, sequences and anticonvulsant activity of contryphan peptides PY 1999 2000 1999 2000

L13 ANSWER 12 OF 19 CA COPYRIGHT 2002 ACS

T1 Gamma-conopeptide agonists for neuronal pacemaker calcium channels PY 1999 1999 1999 2000 2002

L13 ANSWER 13 OF 19 CA COPYRIGHT 2002 ACS

T1 Conotoxin peptides specific for voltage-sensitive sodium channels PY 1998 1998 1996 1996 1999 1998 1999

L13 ANSWER 14 OF 19 CA COPYRIGHT 2002 ACS

T1 .mu.O.-conotoxin M/VIA inhibits mammalian sodium channels, but not through site I PY 1996

L13 ANSWER 15 OF 19 CA COPYRIGHT 2002 ACS

T1 A new family of conotoxins that blocks voltage-gated sodium channels PY 1995

L13 ANSWER 16 OF 19 CA COPYRIGHT 2002 ACS

T1 New Sodium Channel-Blocking Conotoxins Also Affect Calcium Currents in Lymnaea Neurons PY 1995

L13 ANSWER 17 OF 19 CA COPYRIGHT 2002 ACS

T1 Agelenopsis aperta venom and FTX, a purified toxin, inhibit acetylcholine release in Torpedo synaptosomes PY 1993

L13 ANSWER 18 OF 19 CA COPYRIGHT 2002 ACS

T1 Calcium channel antagonist omega-conotoxin binds to intramembrane particles of isolated nerve terminals PY 1993

L13 ANSWER 19 OF 19 CA COPYRIGHT 2002 ACS

T1 Omega-conotoxin differentially blocks acetylcholine and adenosine triphosphate releases from Torpedo synaptosomes PY 1992

(FILE 'HOME' ENTERED AT 13:06:33 ON 17 MAY 2002)

FILE 'REGISTRY' ENTERED AT 13:06:46 ON 17 MAY 2002
L1 38 S CVC CG/ SQSP

FILE 'CA' ENTERED AT 13:07:13 ON 17 MAY 2002
L2 23 S L1

FILE 'REGISTRY' ENTERED AT 13:11:04 ON 17 MAY 2002

E MRCLPVLIIILLLTASAPGVVLPKTE/SQEP

E1 1 MRCLPVEVILLIIILLASVSVDAELKAKDDMPQASPHDNAERDQKKTSDCCFYHNCCG/CSQEP

E2 1 MRCLPVEVILLIIILLTASGSPVDAKVHLKTKGDPLSPFRDNASTLQRLQDKSTC
CGYRMCVPCG/SQEP

E3 0--> MRCLPVLIIILLLTASAPGVVLPKTE/SQEP

E4 1 MRCLPVLIIILLLTASAPGVVLPKTEDDVPMSVVYNGKSLRGILRNGVCCGYKLCHP
C/SQEP

E5 1 MRCLPVLIIILLLTASAPGVVLPKTEDDVPMSVVYNGKSLRGILRNGVCCGYKLCHP
C/SQEP

E6 1 MRCLREGEEVVNHHMAAKIENVCITFSAQAQGITGEIPLWYLFHSTADSLRITAV
SALCRITRHSPTARQNVIEKVLNPVINSLASAICKVQYMLTFTAMLSCGHLQRLQ
EKGFVSTIRLDSPSTICRAKAFVLVLYISYINREMILLSCQSLVMYIERDSRKTTPG
KEQSQNEVYLSKCLDLICH/SQEP

E7 1 MRCLRRPFGWLGMALALACVPAHAESQFAYVYTDLPRKGAKEIIEWMTWR
HOKVGVGYDQVEGRTEVEYGLTDRLOYALYGNVAVARAYHNGPYGATTPPEQFA
DKDVPDARWSGKRFVGVSAEAIYRVLSPYTDGVLAFYVEPTGPQFKELETKV
ILQKNFLDRLITAFNFTYAPEWRYLADDAASGKSW/SQEP

E8 1 MRCLSQEERQEQKEEBERIAENILKRVEAQKRAEMERQKBEERYLEJELQ
RQKEAMRRKKAEEBERLKQMKLCKNKSRLKSLFALSSK/SQEP

E9 1 MRCLTCLKLSFKPLCPNCLNDPLSLKRVYLEGVSVFYAYSEIELIKSKYALIGRI
LPLLQKAGAEFVKILQEOGLNPLYGAIIDDKISFYSAAALKGCQGNLKPTYGRL
RANNAVSVAGKSLERFANNPRNFTFGDESLDYFLDDIITGTTLKEALKYKLTINIKY
HFAIALCSADE/SQEP

E10 1 MRCLITTIMFMFFFLSVIQCKSETSKSGDYIYMGAASSDGDITDNHVELLSLQRS
GKTMRHRVYKHGFSGAHLSEDEAHLAKQPGVLSVFPQMLQLHTTRSWDFLVQESYOR
DTYIETEMNVEQESEMHEGDDTIIGFLDSGIWPEAQSFNDRHMGVPYBEKWGTCMRGKKTQTP
DSFRGNRKLIGARYNNSFF/SQEP

E11 1 MRCLTKTRSFHYVVIIFYSFFLPFLSSSSDDQRTTVSGLFCGRSKSSADPNYIPTFV/S
QEP

E12 1 MRCLTKTRSFHYVVIIFYSFFLPFLSSSSDDQRTTVSGLFCGRSKSSADPNYIPTFVED
MHSLSLKLTRRATESLNSITSIYALQCHDDLSPSDCQLCYAIARTTRIPCLPSSAR
IFLDGCFLEKYEYEFYDESVDSDASDFSCSNDTILDPDRFGQVSETAARVAVRKGFGVYA
GENGVHALLAQWCESLGKEDC/SQEP

L3 2 S MRCLPVLIIILLLTASAPGVVLPKTE/SQSP

FILE 'CA' ENTERED AT 13:14:24 ON 17 MAY 2002
L4 3 S L3

L2 ANSWER 1 OF 23 CA COPYRIGHT 2002 ACS

T1 Cloning and deduced amino acid sequences of 23 human secreted proteins PY 2002

L2 ANSWER 2 OF 23 CA COPYRIGHT 2002 ACS
T1 Protein and cDNA sequences of novel omega-conopeptides from crude *Conus* venom extracts and their therapeutic uses PY 2002

L2 ANSWER 3 OF 23 CA COPYRIGHT 2002 ACS
T1 Genome sequence of the plant pathogen *Ralstonia solanacearum* PY 2002

L2 ANSWER 4 OF 23 CA COPYRIGHT 2002 ACS
T1 Two new classes of conopeptides inhibit the alpha-1-adrenoceptor and noradrenaline transporter PY 2001

L2 ANSWER 5 OF 23 CA COPYRIGHT 2002 ACS
T1 *Propionibacterium* secretes nucleic acids and proteins useful for therapy and diagnosis of acne vulgaris PY 2001 2002 2001 2001 2001 2001

L2 ANSWER 6 OF 23 CA COPYRIGHT 2002 ACS
T1 Novel nucleic acids and protein sequences and its uses PY 2001 2002

L2 ANSWER 7 OF 23 CA COPYRIGHT 2002 ACS
T1 Albumin fusion proteins with therapeutic proteins for improved shelf-life PY 2001

L2 ANSWER 8 OF 23 CA COPYRIGHT 2002 ACS
T1 Nucleic acids and their encoded polypeptides from human bone marrow PY 2001 2001

L2 ANSWER 9 OF 23 CA COPYRIGHT 2002 ACS
T1 Nucleic acids and their encoded polypeptides from human tissues PY 2001 2001 2001 2001

L2 ANSWER 10 OF 23 CA COPYRIGHT 2002 ACS
T1 Cloning and cDNA and deduced amino acid sequences of 43 human secreted proteins PY 2001

L2 ANSWER 11 OF 23 CA COPYRIGHT 2002 ACS
T1 Functional annotation of a full-length mouse cDNA collection PY 2001

L2 ANSWER 12 OF 23 CA COPYRIGHT 2002 ACS
T1 *lambda*-Conotoxins, a new family of conotoxins with unique disulfide pattern and protein folding: isolation and characterization from the venom of *Conus* marmoreus PY 2000

L2 ANSWER 13 OF 23 CA COPYRIGHT 2002 ACS
T1 Human expressed sequence tags and primers for synthesizing full-length cDNAs PY 2001 2002

L2 ANSWER 14 OF 23 CA COPYRIGHT 2002 ACS
T1 Isolation and characterization of a novel *Conus* peptide with apparent antinociceptive activity PY 2000

L2 ANSWER 15 OF 23 CA COPYRIGHT 2002 ACS
T1 Sequence-determined DNA fragments and corresponding encoded polypeptides from corn and *Arabidopsis* PY 2000 2000 2000 2000 2000

L2 ANSWER 16 OF 23 CA COPYRIGHT 2002 ACS
T1 Conotoxin peptides and their use as analgesics PY 2000

L2 ANSWER 17 OF 23 CA COPYRIGHT 2002 ACS
T1 The genome sequence of the plant pathogen *Xylella fastidiosa* PY 2000

L2 ANSWER 18 OF 23 CA COPYRIGHT 2002 ACS
T1 Recombinant cdt-conotoxin peptides for inhibiting neuronal amine transporters PY 2000 2000 2001

L2 ANSWER 19 OF 23 CA COPYRIGHT 2002 ACS
AN 132:103595 CA

T1 Sequence and analysis of chromosome 4 of the plant *Arabidopsis thaliana*

AU Mayer, K.; Schuller, C.; Wambutt, R.; Murphy, G.; Voickaert, G.; Pohl, T.; Dusterhoft, A.; Stiekema, W.; Entian, K.-D.; Teyrn, N.; Harris, B.; Ansoege, W.; Brandt, P.; Gniel, L.; Rieger, M.; Weichsgartner, M.; De Simone, V.; Obermaier, B.; Maché, R.; Müller, M.; Kreis, M.; Delseny, M.; Pliginskij, P.; Watson, M.; Schindlauer, T.; Reichert, B.; Portale, D.; Perez-Alonso, M.; Bouly, M.; Bancroft, I.; Vos, P.; Hohnsbein, J.; Zimmermann, W.; Wedler, H.; Ridley, P.; Langham, S.-A.; McCullagh, B.; Bilham, L.; Robben, J.; Van Der Schueren, J.; Grymoprez, B.; Chang, Y.-J.; Vandenbussche, F.; Braeken, M.; Weljens, J.; Voet, M.; Bastiaens, I.; Aert, R.; Defoor, E.; Weitzenecker, T.; Bothé, G.; Rainsberger, U.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Peters, S.; Van Slaveren, M.; Dirkse, W.; Moolman, P.; Lankhorst, R.; Klein, Rose, M.; Haut, J.; Kotter, P.; Bernier, S.; Hempel, S.; Feldpausch, M.; Lambrecht, S.; Van Den Daele, H.; De Keyser, A.; Buyschaert, C.; Gielens, J.; Villarroel, R.; De Clercq, R.; Van Montagu, M.; Rogers, J.; Cronin, A.; Quail, M.; Bray-Allen, S.; Clark, L.; Doggett, J.; Hall, S.; Kay, M.; Lennard, N.; Mcclay, K.; Mayes, R.; Petitt, A.; Ralandrean, M.-A.; Lyne, M.; Beres, V.; Rechmann, S.; Borkova, D.; Blocker, H.; Scharte, M.; Grimm, M.; Lohrert, T.-H.; Dose, S.; De Haan, M.; Maarse, A.; Schaefer, M.; Müller-Auer, S.; Gabel, C.; Fucini, M.; Farfman, B.; Grandenath, K.; Dauner, D.; Herzl, A.; Neumann, S.; Agirou, A.; Vitale, D.; Liguori, R.; Pravaroli, E.; Massenet, O.; Quigley, F.; Clabaud, G.; Mündlen, A.; Felber, R.; Schnabl, S.; Hiller, R.; Schmidt, W.; Lechamy, A.; Auburg, S.; Chetoui, F.; Cooke, R.; Berger, C.; Montfort, M.; Cascuberta, E.; Gibbons, T.; Weber, N.; Vandenbol, M.; Barques, M.; Teol, J.; Torres, A.; Perez-Perez, A.; Purnelle, B.; Bent, E.; Johnson, S.; Tacon, D.; Jesse, T.; Heijnen, L.; Schwarz, S.; Scholler, P.; Heber, S.; Francis, P.; Biele, C.; Frishman, D.; Haase, D.; Lendke, K.; Mewes, H. W.; Stocker, S.; Zaccaria, P.; Beyan, M.; Wilson, R. K.; De La Bastide, M.; Hebenmann, K.; Parnell, L.; Dedhia, N.; Gnoj, L.; Schutz, K.; Huang, E.; Spiegel, L.; Setkon, M.; Murray, J.; Sheel, P.; Cordes, M.; Abu-Threideh, J.; Stoneking, T.; Kalicki, J.; Graves, T.; Harmon, G.; Edwards, J.;

Latreille, P.; Courtney, L.; Cloud, J.; Abbott, A.; Scott, K.; Johnson, D.; Minx, P.; Bentley, D.; Fulton, B.; Miller, N.; Greco, T.; Kemp, K.; Kramer, J.; Fulton, L.; Mardis, E.; Dante, M.; Pepin, K.; Hillier, L.; Neilson, J.; Spieth, J.; Ryan, E.; Andrews, S.; Giesel, C.; Layman, D.; Du, H.; Ali, J.; Berghoff, A.; Jones, K.; Dione, K.; Cotton, N.; Joshi, C.; Antoniou, B.; Zidanic, M.; Strong, C.; Sun, H.; Lamer, B.; Jordan, C.; Ma, P.; Zhong, J.; Preston, R.; VII, D.; Stekler, M.; Maitro, A.; Shah, R.; Swaby, I.K.; O'Shaughnessy, A.; Rodriguez, M.; Hoffman, J.; Tili, S.; Granat, S.; Shohdy, N.; Hasegawa, A.; Hameed, A.; Lotfi, M.; Johnson, A.; Chen, E.; Marra, M.; Martenssen, R.; McCombe, W. R.

CS GSF-Forschungszentrum f. Umwelt u. Gesundheit, Munich Information Center for Protein Sequences am Max-Planck-Institut f. Biochemie, D-82152, Germany

SO Nature (London) (1999), 402(6763), 769-777 CODEN: NATUAS; ISSN: 0028-0836 PB Macmillan Magazines DT Journal LA English

AB The higher plant *Arabidopsis thaliana* is an important model for identifying plant genes and deq. their function. To assist biol. investigations and to define chromosome structure, a coordinated effort to sequence the *Arabidopsis* genome was initiated in late 1996. This report describes one of the first milestones of this project, the sequence of chromosome 4. Anal. of 17.38 megabases of unique sequence, representing about 17% of the genome, reveals 3744 protein coding genes, 81 fRNAs, and numerous repeat elements. Heterochromatic regions surrounding the putative centromere, which has not yet been completely sequenced, are characterized by an increased frequency of a variety of repeats, new repeats, reduced recombination, lowered gene d., and lowered gene expression. Roughly 60% of the predicted protein-coding genes have been functionally characterized on the basis of their homol. to known genes. Many genes encode predicted proteins that are homologous to human and *Caenorhabditis elegans* proteins. RE CNT 50 THERE ARE 50 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE REFORMAT

IT ***254862-25-4*** RL: BSU (Biological study, unclassified), PRP (Properties), BIOL (Biological study) (amino acid sequence; sequence and anal. of chromosome 4 of the plant *Arabidopsis thaliana*)

RN 254862-25-4 CA

CN Protein (*Arabidopsis thaliana* gene F71N18.30) (9C) (CA INDEX NAME)

SEQ 1 MPPIYGIKLF ROSGASDDVC SKLGIGKEKA LISTAOVQK GNLSGVERE
51 SYGMRNPAPF FAGALGISPE CFAGVCCGG LITLPLQLVI GLLRERPMF
101 ALAAVATAVG WITFPVVA ASTALELYIR SRYSTKD

L2 ANSWER 20 OF 23 CA COPYRIGHT 2002 ACS

AN 131:54612 CA

T1 Complete genome sequence of an aerobic hyper-thermophilic crenarchaeon, *Aeropyrum pernix* K1

AU Kawarabayashi, Yutaka; Hino, Yumi; Honkawa, Hiroshi; Yamazaki, Syuji; Hatahara, Yui; Jin-No, Koji; Takahashi, Mikio; Sekine, Mitsuo; Baba, Shin-ichi; Aikai, Akiro; Kosugi, Hiroki; Hosoyama, Akira; Fukui, Shigeohji; Nagai, Yoshimi; Nishijima, Keiko; Nakazawa, Hidekazu; Takamiya, Mitsuaki; Masuda, Sayaka; Funahashi, Tomonobu; Tanaka, Toshihiro; Kudoh, Yutaka; Yamazaki, Jun; Kushiida, Norihito; Oguchi, Aiko; Aoki, Ken-ichi; Kubota, Kenji; Nakamura, Yoshinobu; Nomura, Norimichi; Sako, Yoshinori; Kikuchi, Hisasi

CS National Institute of Technology and Evaluation, Tokyo, 151-0066, Japan

SO DNA Research (1999), 6(2), 83-101, 145-152 CODEN: DARSEB; ISSN: 1340-2838 PB Universal Academy Press DT Journal LA English

AB The complete sequence of the genome of an aerobic hyper-thermophilic crenarchaeon, *Aeropyrum pernix* K1, which optimally grows at 95 degree., was dectd. by the whole genome shotgun method with some modifications. The entire length of the genome was 1,669,695 bp. The authenticity of the entire sequence was supported by restriction anal. of long PCR products, which were directly amplified from the genomic DNA. As the potential protein-coding regions, a total of 2694 open reading frames (ORFs) were assigned. By similarly search against public databases, 633 (23.5%) of the ORFs were related to genes with putative function and 523 (19.4%) to the sequences registered but with unknown function. All the genes in the TCA cycle except for that of alpha-ketoglutarate dehydrogenase were included, and instead of the alpha-ketoglutarate dehydrogenase gene, the genes coding for the 2 subunits of 2-oxoacid:ferredoxin oxidoreductase were identified. The remaining 1538 ORFs (37.1%) did not show any significant similarity to the sequences in the databases. Sequence comparison among the assigned ORFs suggested that a considerable member of ORFs were generated by sequence duplication. The RNA genes identified were a single 16S-23S rRNA operon, two 5S rRNA genes, and 47 rRNA genes including 14 genes with intron structures. All the assigned ORFs and RNA coding regions occupied 89.12% of the whole genome. The data presented in this paper are available on the internet homepage (<http://www.milid.nite.go.jp>) RE CNT 23 THERE ARE 23 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE REFORMAT

IT ***227778-77-0*** RL: BSU (Biological study, unclassified), PRP (Properties), BIOL (Biological study) (amino acid s-sequence; complete genome sequence of *Aeropyrum pernix* K1)

RN 227778-77-0 CA

CN 130Aa long protein (*Aeropyrum pernix* strain K1 gene APE2083) (9C) (CA INDEX NAME)

S EQ 1 MRCCEDLASR HYLAAVIYP YPPNPERVY CAAGHSQLG GLAEOGHLL
51 LPLGLPLPGS DRIVLMQLQR SNMELLEQ PHTSLRKAG GRVCCORPPO

101 AALTIPLHEQLRQGRPRPAT PSHLPVGVCCG

L2 ANSWER 21 OF 23 CA COPYRIGHT 2002 ACS

AN 130:333763 CA

T1 Cloning and cDNA and deduced amino acid sequences of 125 human secreted proteins

IN Feng, Ping; Carter, Kenneth C.; Endress, Gregory A.; Rosen, Craig A.; Ruben, Steven M.; Janat, Fouad; Ni, Jian; Wei, Ying-Fei; Moore, Paul A.; Soppet, Daniel R.; Kyaw, Hla; Lalleur, David W.; Olsen, Henrik S.; Shi, Yanguu; Ebner, Reinhard

SO Human Genome Sciences, Inc., USA; et al.

SA PCT Int. Appl., 507 pp. CODEN: PXXD2 DT Patent LA English

FAN CNT 2 PATENT NO. KIND DATE APPLICATION NO. DATE _____

PI WO 9924236 A1 19990520 WO 1998-US23435 19981104 W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, GR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG CA 2308768 AA 19990520 CA 1998-2308768 19981104 AU 9913037 A1 19990531 AU 1999-13037 19981104 EP 1032338 A1 20000906 EP 1998-956533 19981104 R: AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT, IE, FI

PRAI US 1997-64908P P 19971107 US 1997-64908P P 19971107 US 1997-64911P P 19971107 US 1997-64912P P 19971107 US 1997-64983P P 19971107 US 1997-64984P P 19971107 US 1997-64985P P 19971107 US 1997-64987P P 19971107 US 1997-64988P P 19971107 US 1997-66089P P 19971117 US 1997-66090P P 19971117 US 1997-66094P P 19971117 US 1997-66095P P 19971117 US 1997-66100P P 19971117 WO 1998-US23435 W 19981104

AB The present invention relates to 125 novel human secreted proteins and isolated nucleic acids sites, the coding regions of the genes encoding such proteins. Tissue distribution, sequence homologies, and preferred epitope sites are provided for the secreted proteins, as well as chromosomal mapping of some of the genes. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins in bacterial, insect, and mammalian cells. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins. High-throughput screening assays are also provided for various putative activities of the secreted proteins. RE CNT 4 THERE ARE 4 CITED REFERENCES AVAILABLE FOR THIS RECORD ALL CITATIONS AVAILABLE IN THE REFORMAT

IT ***224311-30-2P*** RL: BOC (Biological occurrence), BPN (Biosynthetic preparation), BSU (Biological study, unclassified), PRP (Properties), THU (Therapeutic use), BIOL (Biological study), OCCU (Occurrence), PREP (Preparation), USES (Uses) (amino acid sequence; cloning and cDNA and deduced amino acid sequences of 125 human secreted proteins)

RN 224311-30-2 CA

CN Secretory protein (human clone HNF1R81 59-amino acid precursor) (9C) (CA INDEX NAME)

SEQ 1 MELWFRFLHLMLPRGVCC GICVCVRGGM VLSEPTSCGG RALSCGEGCH 51 SGRVQFRPRP

L2 ANSWER 22 OF 23 CA COPYRIGHT 2002 ACS

AN 128:176689 CA

T1 The complete nucleotide sequence and functional organization of *Bacillus subtilis* bacteriophage SPP1

AU Alonso, Juan C.; Luder, Gerhild; Stige, Asila C.; Chai, Sunghae; Weise, Frank; Trautner, Thomas A.

CS Centro Nacional Biotecnologia, CSIC, Campus Universidad Autonoma Madrid, Madrid, 28049 Spain

SO Gene (1997), 204(1/2), 201-212 CODEN: GENED6; ISSN: 0378-1119 PB Elsevier Science B.V. DT Journal LA English

AB The complete nucleotide sequence of the B. subtilis bacteriophage SPP1 is described. The genome is 44 007 bp in size and has a base compn. of 43.7% dG+dC. Only 32.2 kb are essential for phage amplification under lab. conditions. Transcription using only the 'heavy strand' is asym. Eight-one orfs organized in five early and four late operons were identified. Expts. have shown that 25 orfs are essential. Of the remaining orfs, functions could be predicted for the products of five of the orfs on the basis of comparison of the deduced amino acid sequence to known proteins. Intergenic regions include most of the 5' P1 and the 4' P1 promoters. Transcripts are polycistronic. Transcription from the P1 promoters is mediated by host RP, whereas recognition of the P1 promoters requires an addnl. unidentified phage-encoded product. Translation of mRNA transcribed from most of the orfs seems to be initiated independently, each from its own ribosomal binding and initiation site, although a few cases of coupled translation have been reported. The organization of SPP1 genes involved in the replication, DNA packaging and phage assembly proteins resembles the organization of genes of equiv. regions of different E. coli double-stranded DNA phages. Absence of aa sequence similarity between analogous proteins of different phages suggested that the conserved gene organization is representative of a primordial bacteriophage. IT ***203011-09-0*** RL: BSU (Biological study, unclassified), PRP (Properties), BIOL (Biological study) (amino acid sequence; complete nucleotide sequence and functional organization of *Bacillus subtilis* bacteriophage SPP1)

RN 203011-09-0 CA

CN Protein (Bacillus phage SP1 gene 3.1, reduced) (9CI) (CA INDEX NAME)

SEQ 1 MRGMWEMAKI ESMTIKEFNM RGKANVTVD VNFPPYKKRT FIKASLPFL
51 ILPKSALAAG IDSTFGNVHG AIMNAFDAGV VLVIIFAGAA WGLGNRTQAI
101 EILGVCCGY ILARHAVDVR DFLRGI

L2 ANSWER 23 OF 23 CA COPYRIGHT 2002 ACS

AN 112:113311 CA

TI Vasotocin genes of the teleost fish *Catostomus commersoni*: gene structure, exon-intron boundary, and hormone precursor organization

AU Morley, Steven D.; Schoenrock, Christiane; Heierhorst, Joerg; Figueroa, Jaime; Lederfs, Karl; Richter, Dietmar

CS Inst Zellbiochem., Univ. Hamburg, Hamburg, 2000/20, Fed. Rep. Ger.

SO Biochemistry (1990), 29(10), 2506-11 CODEN: BICHAW; ISSN: 0006-2960 DT Journal LA English

AB Some cDNA clones encoding 2 members of the vasotocin hormone precursor gene family were isolated from the white sucker *C. commersoni*. The hormone is encoded by 2 distinct genes, both of which are expressed, as indicated by Northern blot anal. Genomic DNA amplified by the polymerase chain reaction has been used to define exon-intron boundaries. Both vasotocin genes contain introns in positions corresponding to those found in the gene of their mammalian counterpart vasopressin. The predicted vasotocin precursors show a surprising degree of sequence divergence, amounting to 45% at the amino acid level, of which only .apprx. 1/2 can be accounted for by conservative amino acid changes. The precursors include a

hormone moiety, followed by a putative neurophysin sequence, that is longer at the C-terminus by a tract of some 30 amino acids by comparison to their mammalian counterpart. Each of these sequences contains a leucine-rich core segment resembling that found in copeptin, a glycopeptide moiety present in mammalian vasopressin precursors.

IT ****125048-72-8****, Vasotocin (*Catostomus commersoni* precursor isoform 2, reduced) RL: PRP (Properties) (amino acid sequence of)

RN 125048-72-8 CA

CN Vasotocin (*Catostomus commersoni* precursor isoform 2, reduced) (9CI) (CA INDEX NAME)

SEQ 1 MSYCAVLLLC VAGLLQLSSA CYIQNCPRRGG KRALLEPVSR OCLACGPGBK

51 GRCLGPSICC GEEIGCLVGS PMWARCOEEE YLPSPCQTAG KLCSDAGPC

101 AAPGVCCGTE GCKLDPNCSE DSESEEPADQ NTLGASPGEL LLRLHPNNR

151 KHNQY

L4 ANSWER 1 OF 3 CA COPYRIGHT 2002 ACS

TI Isolation and characterization of a novel *Conus* peptide with apparent antinociceptive activity PY 2000

L4 ANSWER 2 OF 3 CA COPYRIGHT 2002 ACS

TI Conotoxin peptides and their use as analgesics PY 2000

L4 ANSWER 3 OF 3 CA COPYRIGHT 2002 ACS

TI Recombinant ch1-conotoxin peptides for inhibiting neuronal amine transporters PY 2000 2000 2001